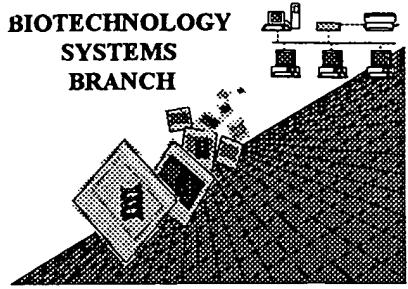


Shukla

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

BEST AVAILABLE COPY

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/357,675
Art Unit / Team No.: 1632
Date Processed by STIC: 11/9/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/357,675

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

Shukla

1632

PAGE : 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/357,675

DATE: 11/09/1999
TIME: 11:27:24

Input Set: I357675.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

1 <110> APPLICANT: Croce M.D., Carlo M.
2 <120> TITLE OF INVENTION: Nitrilase Homologs
3 <130> FILE REFERENCE: CRO01 NP001 Nitrilase Homologs
4 <140> CURRENT APPLICATION NUMBER: US/09/357,675
5 <141> CURRENT FILING DATE: 1999-07-20
6 <150> EARLIER APPLICATION NUMBER: 60/093,350
7 <151> EARLIER FILING DATE: 1998-07-20
8 <160> NUMBER OF SEQ ID NOS: 18
9 <170> SOFTWARE: PatentIn Ver. 2.1
10 <210> SEQ ID NO 1
11 <211> LENGTH: 1416
12 <212> TYPE: DNA
13 <213> ORGANISM: Homo sapiens
14 <400> SEQUENCE: 1 *see item 10 on E*

Does Not Comply
Corrected Diskette Needed

see p. 2, too

^s see item 10 on Error Summary Sheet

W-->

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19 aactgcccct ggtggctgtg tgccaggtaa catgcacgcc agacaagcaa cagaacttta 300
20 aaacatgtgc tgagctggtt cgagaggctg ccagactggg tgcctgcctg gctttcctgc 360
21 ctgaggcatt tgacttcatt gcacgggacc ctgcagagac gctacacctg tctgaaccac 420
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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/357,675

DATE: 11/09/1999
 TIME: 11:27:24

Input Set: I357675.RAW

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PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/357,675DATE: 11/09/1999
TIME: 11:27:24

Input Set: I357675.RAW

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137 <212> TYPE: DNA
138 <213> ORGANISM: Homo sapiens
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VERIFICATION SUMMARY
PATENT APPLICATION US/09/357,675DATE: 11/09/1999
TIME: 11:27:24

Input Set: I357675.RAW

Line ? Error/Warning

Original Text

15 W "N" or "Xaa" used: Feature required
56 W "N" or "Xaa" used: Feature required
62 W "N" or "Xaa" used: Feature required

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